Tribute to Michael Waterman on His 67th Birthday

It is with great delight that we dedicate this volume of *Communications in Information and Systems* to Professor Michael Waterman on the occasion of his 67th birthday.

There is an evolutionary trajectory of theories, collaborations, and mentoring in an enchanting environmental niche that reaches to one common-ancestor node. It was John von Neumann who proposed a research program aimed at a new computation and information theory essential for modeling the biological systems of the cell. The overarching goal of his new theory was the unification of continuous and discrete mathematics via the concept of statistical thermodynamic error. The two pillars to be unified via mathematical statistics were continuous mathematics, namely mathematical analysis, "the technically most successful and best-elaborated part of mathematics," and discrete mathematics, which "deals with rigid, all-or-none concepts, and has very little contact with the continuous concept of the real or complex number … technically most refractory parts of mathematics … by the nature of its approach, cut off from the best cultivated portions of mathematics, and forced onto the most difficult part of mathematical terrain, into combinatorics."

It just so happened that John von Neumann brought Stan Ulam to New Mexico, Stan Ulam brought Bill Beyer to New Mexico, Bill Beyer brought Michael Waterman to New Mexico, and Michael Waterman brought many of us to New Mexico when in 1997 he started the Annual International Conference on Research in Computational Biology, the RECOMB Conference. Carrying the torch from mathematicians in love with biology at the end of the 20th century and the start of the 21st, Michael Waterman stood there at the first RECOMB conference in Santa Fe, surrounded by Bill Beyer and Nick Metropolis, two surviving members of the greatest generation of mathematicians in residence in New Mexico, the Land of Enchantment, and declared: "This volume [the first RECOMB Proceedings] is proof positive of the vitality of a new discipline: *computational biology*."

The collection of papers in the present volume is indeed a beautiful exemplification of Mike Waterman's pioneering influence, trailblazing new areas of research through a wide range of computational and mathematical methods applied to biological problems, intertwining statistical and algorithmic methods towards a genuine statistics-powered continuous-discrete hybrid that would have passed the von Neumann test.

In the area of *strings, alignment and rearrangements*, Alberto Apostolico presents advances in pattern matching; Leming Zhou, Ingrid Mihai and Liliana Florea focus on methods for space seeds for cDNA to genome alignment; and Qian Peng, Max A. Alekseyev, Glenn Tesler and Pavel A. Pevzner develop algorithms for the genomic architecture of mammalian and plant genomes. Several papers are devoted to *SNPs, haplotypes and associations:* Yang-Ho Chen and Ting Chen consider combinatorial optimization methods for tagging SNPs; Dan Gusfield and Yufeng Wu show the complexity of three-state perfect phylogeny; Russell Schwartz surveys haplotype assembly algorithmics; Ofir Davidovich, Gad Kimmel, Eran Halperin and Ron Shamir consider tradeoffs in power, imputation, and tagging SNPs in association studies; Sudeep Srivastava and

Liang Chen study model selection in association studies; and Lin Wan, Yi Xiao, Quan Chen, Minghua Deng and Minping Qian present methods for copy number analysis based on SNP arrays.

In *next-generation sequencing,* Margaret Taub, Doron Lipson and Terence P. Speed focus on statistical modeling of removing bias from short read assignments to the genome, and Rui Jiang, Ting Chen and Fengzhu Sun discuss Bayesian and Gibbs sampling strategies for network motif identification in stochastic networks, part of the area of *biological networks.* In the area of *RNA and proteins,* Lydia Tapia, Shawna Thomas and Nancy M. Amato study molecular motion of proteins and RNA, and Sorin Istrail and Fumei Lam survey mathematical results for combinatorial algorithms for protein folding. Two papers present research in the area of *behavior phenotype and phenotype prediction:* Dhruv Grover and Simon Tavare describe methods for studying behavior of *Drosophila melanogaster,* and Nir Yosef, Jens Gramm, Qian-fei Wang, William S. Noble, Richard M. Karp and Roded Sharan presents methods for genotype-phenotype prediction.

From Los Angeles to Beijing, from Tel-Aviv to Providence and San Diego, and from the international world of computational biology, we wish you: Happy Birthday, Michael!

Guest Editors:

Sorin Istrail, Brown University
Pavel Pevzner, University of California, San Diego
Ron Shamir, Tel-Aviv University
Fengzhu Sun, University of Southern California